

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,

5 (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
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(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 92037

15 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

20 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 30-AUG-1991
(C) CLASSIFICATION:

25 (vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Wetherell, Jr. Ph.D., John W.
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-1294

30 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619-455-5100
(B) TELEFAX: 619-455-5110

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DB60R32

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 130..1177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CCCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG      60
15 CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA      120
GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC      168
    Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe
        1             5             10

20 GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC      216
    Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys
        15             20             25

    AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG      264
    Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala
        30             35             40             45

25 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC      312
    Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala
        50             55             60

    AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC      360
    Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His
        65             70             75

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	AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC	408
	Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly	
	80 85 90	
5	GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG	456
	Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val	
	95 100 105	
	TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG	504
	Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr	
	110 115 120 125	
10	TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT	552
	Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val	
	130 135 140	
	CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC	600
15	Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro	
	145 150 155	
	GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC	648
	Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr	
	160 165 170	
20	GTG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC	696
	Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly	
	175 180 185	
	CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG	744
	Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu	
	190 195 200 205	
25	TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT	792
	Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val	
	210 215 220	
	ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC	840
30	Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys	
	225 230 235	
	ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC	888
	Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly	
	240 245 250	

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	AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG	936
	Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu	
	255 260 265	
5	CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA	984
	Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly	
	270 275 280 285	
	GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG	1032
	Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu	
	290 295 300	
10	CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG	1080
	Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met	
	305 310 315	
	ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT	1128
15	Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn	
	320 325 330	
	GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T	1177
	Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala	
	335 340 345	
	GAAGCCAGAG AGTGAGAGAC ATTAAGTCAT TAGACTGGAA CTTGAACTGA TTCACATCTC	1237
20	ATTTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTAA AATCTGTTTT TCTAACTGGG	1297
	GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC	1357
	CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGG ACTACATTAG TACACAGCAC	1417
	CAGAAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT	1477
	CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA	1537
25	AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC	1597
	CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA	1657
	CATTCTGATT CGAATGACAC TGTTCAAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT	1717
	TGTGGCAAGT GAATTTCCT GTAACAAGCC AGATTTTTTA AAATTATAT TGTAATATT	1777
	GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTAA	1837

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AGTIGTTTGT GCCTTTTAT TTTTGT TTTT AATGCTTTGA TATTTC AATG TTAGCCTCAA 1897
 TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT 1957
 ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA 2017
 GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCAGG 2075

5 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
 1 5 10 15
 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
 20 25 30
 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
 35 40 45
 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50 55 60
 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 65 70 75 80
 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85 90 95
 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100 105 110
 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115 120 125

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Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130 135 140
 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145 150 155 160
 5 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165 170 175
 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180 185 190
 10 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195 200 205
 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210 215 220
 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225 230 235 240
 15 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245 250 255
 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260 265 270
 20 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275 280 285
 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
 290 295 300
 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
 305 310 315 320
 25 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
 325 330 335
 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345